



APR 25 2002

TECH CENTER 1600/2900

SEQUENCE LISTING

<110> Yang, Chu-Wen
Tsou, Ann-Ping
Chi, Chin-Wen
Fann, Ming-Ji
Chou, Chen-Kung

<120> CELL CYCLE REGULATOR PROTEIN

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>210> 2

>211> 808

>212> PRT

>213> Mus musculus

>400> 2

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 50          55          60
Thr Ser Gln Asp Leu Ser Pro Glu Lys Ala Ser Ser Lys Thr Arg Ser
 65          70          75          80
Val Lys Met Val Leu Ser Asp Gln Arg Lys Gln Leu Leu Gln Lys Tyr
 85          90          95
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100          105          110
Lys Arg Gly Val Phe Lys Val Gly Leu Tyr Arg Pro Ala Ala Pro Gly
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Lys Val Ile Pro Ser Lys Val Glu Arg Asp Glu Lys His Leu Asp Ser
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 Asp Leu Ile Leu Phe Ser Pro Leu
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4210 • 3
 4211 • 2538
 4212 • DNA
 4213 • Homo sapiens

4400 • 3
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2538

0210: 4

0211: 846

0212: PRT

0213: Homo sapiens

0400: 4

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Ala	Lys	Arg	Gly	Ile	Phe	Lys	Val	Gly	Arg	Tyr	Arg	Pro	Asp	Met	Pro
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Pro	Gly	Pro	Arg	Gln	Thr	Ser	Glu	Lys	Lys	Val	Ser	Asp	Lys	Glu	Lys
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 Ser Glu Arg Met Ser Leu Pro Leu Leu Ala Gly Gly Val Ala Asp Asp
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 755 760 765
 Glu Lys Asn Thr Ala Ser Gln Asn Ser Ile Leu Glu Glu Gly Glu Thr
 770 775 780
 Lys Ile Ser Gln Ser Glu Leu Phe Asp Asn Lys Ser Leu Thr Thr Glu
 785 790 795 800
 Cys His Leu Leu Asp Ser Pro Gly Leu Asn Cys Ser Asn Pro Phe Thr
 805 810 815
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*210> 5
 *211> 2966
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*220>
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 *222> (301)...(2724)

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Lys Glu Glu Lys Gln Leu Gln Lys Leu Lys Glu Gln Arg Glu Lys Ala	
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Phe Leu Val Thr Asp Gln Arg Gly Ala Lys Ala Glu Pro Glu Lys Ala	
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Lys Val Ile Pro Ser Lys Val Glu Arg Asp Glu Lys His Leu Asp Ser	260 265 270	
cag acc agg gaa aca agt gaa atg ggt ctg ctg gga gtc ttc cga gaa		1164
Gln Thr Arg Glu Thr Ser Glu Met Gly Leu Leu Gly Val Phe Arg Glu	275 280 285	
gtg gaa agc ttg cct gca aca gcc cct gcc caa gga aag gaa agg aag		1212
Val Glu Ser Leu Pro Ala Thr Ala Pro Ala Gln Gly Lys Glu Arg Lys	290 295 300	
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Ser Phe Ala Pro Lys His Cys Val Phe Gln Pro Pro Cys Gly Leu Lys	305 310 315 320	
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Ser Tyr Gln Val Ala Pro Leu Ser Pro Arg Ser Ala Asn Ala Phe Leu	325 330 335	
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Thr Pro Asn Cys Asp Trp Asn Gln Leu Arg Pro Glu Val Phe Ser Thr	340 345 350	
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Thr Thr Gln Asp Lys Ala Asn Glu Ile Leu Val Gln Gln Gly Leu Glu	355 360 365	
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Ser Leu Thr Asp Arg Ser Lys Glu His Val Leu Asn Gln Lys Gly Ala	370 375 380	
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Ser Thr Ser Asp Ser Asn His Ala Ser Val Lys Gly Val Pro Cys Ser		

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Glu Gly Ser Glu Gly Gln Thr Ser Gln Pro Pro His Asp Val Pro Tyr				
405		410	415	
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Phe Arg Lys Ile Leu Gln Ser Glu Thr Asp Arg Leu Thr Ser His Cys				
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Leu Glu Trp Glu Gly Lys Leu Asp Leu Asp Ile Ser Asp Glu Ala Lys				
435		440	445	
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Gly Leu Ile Arg Thr Thr Val Gly Gln Thr Arg Leu Leu Ile Lys Glu				
450		455	460	
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Arg Phe Arg Gln Phe Glu Gly Leu Val Asp Asn Cys Glu Tyr Lys Arg				
465		470	475	480
ggt gaa aag gag aag acc tgc acc gat ctg gat gga ttc tgg gat atg				174
Gly Glu Lys Glu Thr Thr Cys Thr Asp Leu Asp Gly Phe Trp Arg Met				
485		490	495	
gtt agt ttt cag gtc gat gat gtg aac cag aaa ttc aac aac ctg atc				1836
Val Ser Phe Gln Val Asp Asp Val Asn Gln Lys Phe Asn Asn Leu Ile				
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Lys Leu Glu Ala Ser Gly Trp Lys Asp Ser Asn Asn Pro Ser Lys Lys				
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Val Leu Arg Lys Lys Ile Val Pro Gly Arg Thr Ser Lys Ala Lys Gln				
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Asn Ala Met Lys Gly Arg Pro Gln Gln Glu Val Gln Ala His Ala Ala				
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Ala Pro Glu Thr Thr Lys Glu Val Asp Lys Ile Val Phe Asp Ala Gly				
580		585	590	
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Phe Phe Arg Ile Glu Ser Pro Val Lys Ser Phe Ser Val Leu Ser Ser				
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Thr Phe Ser Asp Gly Leu Glu Ser Arg Cys His Val Glu Asp Thr Pro
660 665 670

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Cys Pro Gly Glu Gln Asp Ser Ser Asp Ile Glu His Asp Val Asn Lys
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Ile Asn Val Lys Met Asp Cys Phe Ser Val Glu Thr Asn Leu Pro Leu
690 695 700

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740 745 750

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755 760 765

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His Leu Leu Glu Pro Pro Gly Leu Ser Cys Thr Ser Pro Cys Thr Arg
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785 790 795 800

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Asp Leu Ile Leu Phe Ser Pro Leu
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0220 *

0221 * CDS

0222 * (218)...(2755)

0400 * 6

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				Met	Ser Ser Ser His Phe	
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Ala	Ser	Arg	His	Arg	Lys	Asp	Ile	Ser	Thr	Glu	Met	Ile	Arg	Thr	Lys	
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Ile	Ala	His	Arg	Lys	Ser	Leu	Ser	Gln	Lys	Glu	Asn	Arg	His	Lys	Glu	
		25				30					35					

tac	gaa	cga	aat	aga	cac	ttt	ggc	ttg	aaa	gat	gta	aac	att	cca	acc	379
Tyr	Glu	Arg	Asn	Arg	His	Phe	Gly	Leu	Lys	Asp	Val	Asn	Ile	Pro	Thr	
	40				45					50						

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Leu	Glu	Gly	Arg	Ile	Leu	Val	Glu	Leu	Asp	Glu	Thr	Ser	Gln	Glu	Leu	
	55				60				65					70		

gtt	cca	gaa	aag	acc	aat	gtt	aag	cca	arg	gca	atg	aaa	act	att	cta	475
Val	Pro	Glu	Lys	Thr	Asn	Val	Lys	Pro	Arg	Ala	Met	Lys	Thr	Ile	Leu	
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Gly	Asp	Gln	Arg	Lys	Gln	Met	Leu	Gln	Lys	Tyr	Lys	Glu	Glu	Lys	Gln	
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ctt	caa	aaa	ttg	aaa	gag	cag	aga	gag	aaa	gct	aaa	cga	gga	ata	ttt	571
Leu	Gln	Lys	Leu	Lys	Glu	Gln	Arg	Glu	Lys	Ala	Lys	Arg	Gly	Ile	Phe	
	105					110						115				

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Lys	Val	Gly	Arg	Tyr	Arg	Pro	Asp	Met	Pro	Cys	Phe	Leu	Leu	Ser	Asn	
	120					125					130					

cag	aat	gct	gtg	aaa	gct	gag	cca	aaa	aag	gct	att	cca	tct	tct	gta	667
Gln	Asn	Ala	Val	Lys	Ala	Glu	Pro	Lys	Lys	Ala	Ile	Pro	Ser	Ser	Val	
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cgg	att	aca	agg	tca	aag	goc	aaa	gac	caa	atg	gag	cag	act	aag	att	715
Arg	Ile	Thr	Arg	Ser	Lys	Ala	Lys	Asp	Gln	Met	Glu	Gln	Thr	Lys	Ile	
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gat	aac	gag	agt	gat	gtt	cga	gca	atc	cga	cct	ggc	cca	aga	caa	act	763
Asp	Asn	Glu	Ser	Asp	Val	Arg	Ala	Ile	Arg	Pro	Gly	Pro	Arg	Gln	Thr	
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Ser Glu Lys Lys Val Ser Asp Lys Glu Lys Lys Val Val Gln Pro Val	
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Met Pro Thr Ser Leu Arg Met Thr Arg Ser Ala Thr Gln Ala Ala Lys	
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Gln Val Pro Arg Thr Val Ser Ser Thr Thr Ala Arg Lys Pro Val Thr	
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235 240 245	
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Arg Pro Ala Lys Asn Val Glu Thr Lys Pro Asp Lys Gly Ile Ser Cys	
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Lys Val Asp Ser Glu Glu Asn Thr Leu Asn Ser Gln Thr Asn Ala Thr	
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Ser Gly Met Asn Pro Asp Gly Val Leu Ser Lys Met Glu Asn Leu Pro	
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Pro Met Thr Pro Arg Ser Ala Asn Ala Phe Leu Thr Pro Ser Tyr Thr	
330 335 340	
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Trp Thr Pro Leu Lys Thr Glu Val Asp Glu Ser Gln Ala Thr Lys Glu	
345 350 355	
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Ile Leu Ala Gln Lys Cys Lys Thr Tyr Ser Thr Lys Thr Ile Gln Gln	
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Asp Ser Asn Lys Leu Pro Cys Pro Leu Gly Pro Leu Thr Val Trp His	
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Leu Glu Leu Asp Ile Pro Asp Asp Ala Lys Asp Leu Ile Arg Thr Ala	
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Val Gly Gln Thr Arg Leu Leu Met Lys Glu Arg Phe Lys Gln Phe Glu	
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Cys Thr Asp Leu Asp Gly Phe Trp Asp Met Val Ser Phe Gln Ile Glu	
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Trp Gln Val Asn Asn Asn Met Asn His Asn Met Asn Lys Asn Val Phe	
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Arg Lys Lys Val Val Ser Gly Ile Ala Ser Lys Pro Lys Gln Asp Asp	
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Orf 1